Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/662,786

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. **If intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) 1-4 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n/Xaa	"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

OIPE

RAW SEQUENCE LISTING DATE: 09/25/2003
PATENT APPLICATION: **US/10/662,756** TIME: 16:04:46

Input Set : **A:\REG660AZ.txt**
Output Set: **N:\CRF4\09252003\J662756.raw**

```
     4 <110> APPLICANT: Economides et al.
     6 <120> TITLE OF INVENTION: DCR-5 BONE AFFECTING LIGAND
     8 <130> FILE REFERENCE: REG 660-A-PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/662,756
C--> 11 <141> CURRENT FILING DATE: 2003-09-15
    13 <150> PRIOR APPLICATION NUMBER: 60/097,296
    14 <151> PRIOR FILING DATE: 1998-08-20
    16 <160> NUMBER OF SEQ ID NOS: 21
    18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
    20 <210> SEQ ID NO: 1
    21 <211> LENGTH: 27
    22 <212> TYPE: DNA
    23 <213> ORGANISM: Artificial Sequence
    25 <220> FEATURE:
    26 <221> NAME/KEY: misc_feature
    27 <222> LOCATION: 3, 12, 18
    28 <223> OTHER INFORMATION: n = A, T, C or G
    30 <400> SEQUENCE: 1
W--> 31  mgn aar tay ytn aar wsn gay tgg tgy                          27
    33 <210> SEQ ID NO: 2
    34 <211> LENGTH: 24
    35 <212> TYPE: DNA
    36 <213> ORGANISM: Artificial Sequence
    38 <220> FEATURE:
    39 <221> NAME/KEY: misc_feature
    40 <222> LOCATION: 6, 9, 12, 21
    41 <223> OTHER INFORMATION: n = A,T,C or G
    43 <400> SEQUENCE: 2
W--> 44  caracngtnw sngargargg ntgy                                   24
    46 <210> SEQ ID NO: 3
    47 <211> LENGTH: 21
    48 <212> TYPE: DNA
    49 <213> ORGANISM: Artificial Sequence
    51 <220> FEATURE:
    52 <221> NAME/KEY: misc_feature
    53 <222> LOCATION: 1, 4, 10, 13, 16
    54 <223> OTHER INFORMATION: n = A, T, C or G
    56 <400> SEQUENCE: 3
W--> 57  nggnggrtcn arnccnggrc a                                      21
    59 <210> SEQ ID NO: 4
    60 <211> LENGTH: 24
    61 <212> TYPE: DNA
    62 <213> ORGANISM: Artificial Sequence
```

pp 1-3
Does Not Comply
Corrected Diskette Needed
Needs explanation - see item 11 on Error Summary Sheet

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```
     64 <220> FEATURE:
     65 <221> NAME/KEY: misc_feature
     66 <222> LOCATION: 1, 7, 10, (10) 19
     67 <223> OTHER INFORMATION: n = A, T, C or G
     69 <400> SEQUENCE: 4
W--> 70  narrttnacn swcatrcanc krca                                        24
     72 <210> SEQ ID NO: 5
     73 <211> LENGTH: 192
     74 <212> TYPE: DNA
     75 <213> ORGANISM: Homo sapiens
     77 <220> FEATURE:
     78 <221> NAME/KEY: CDS
     79 <222> LOCATION: (1)...(192)
     81 <400> SEQUENCE: 5
     82  cag aca gtg acg gag gag ggc tgc cgg agc cgc acc atc ctc aac cgc       48
     83  Gln Thr Val Thr Glu Glu Gly Cys Arg Ser Arg Thr Ile Leu Asn Arg
     84   1               5                  10                  15
     86  ttc tgc tac ggc cag tgc aac tcc ttc tac atc ccg cgg cac gtg aag       96
     87  Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro Arg His Val Lys
     88              20                  25                  30
     90  aag gag gag gag tcc ttc cag tcc tgc gcc ttc tgc aag ccc cag cgc      144
     91  Lys Glu Glu Glu Ser Phe Gln Ser Cys Ala Phe Cys Lys Pro Gln Arg
     92          35                  40                  45
     94  gtc acc tcc gtc ctc gtg gag ctc gag tgc ccg gga cta gac ccc cca      192
     95  Val Thr Ser Val Leu Val Glu Leu Glu Cys Pro Gly Leu Asp Pro Pro
     96      50                  55                  60
     99 <210> SEQ ID NO: 6
    100 <211> LENGTH: 64
    101 <212> TYPE: PRT
    102 <213> ORGANISM: Homo sapiens
    104 <400> SEQUENCE: 6
    105  Gln Thr Val Thr Glu Glu Gly Cys Arg Ser Arg Thr Ile Leu Asn Arg
    106   1               5                  10                  15
    107  Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro Arg His Val Lys
    108              20                  25                  30
    109  Lys Glu Glu Glu Ser Phe Gln Ser Cys Ala Phe Cys Lys Pro Gln Arg
    110          35                  40                  45
    111  Val Thr Ser Val Leu Val Glu Leu Glu Cys Pro Gly Leu Asp Pro Pro
    112      50                  55                  60
    116 <210> SEQ ID NO: 7
    117 <211> LENGTH: 30
    118 <212> TYPE: DNA
    119 <213> ORGANISM: Artificial Sequence
    121 <220> FEATURE:
    122 <223> OTHER INFORMATION: Primer
    124 <400> SEQUENCE: 7
    125  agc cgc acc atc ctc aac cgc ttc tgc tac                             30
    127 <210> SEQ ID NO: 8
    128 <211> LENGTH: 10
```

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```
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Primer
135 <400> SEQUENCE: 8
136  Ser Arg Thr Ile Leu Asn Arg Phe Cys Tyr
137   1               5                  10
139 <210> SEQ ID NO: 9
140 <211> LENGTH: 27
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Primer
147 <400> SEQUENCE: 9
148  ctcgagctcc acgaggacgg aggtgac                                          27
150 <210> SEQ ID NO: 10
151 <211> LENGTH: 9
152 <212> TYPE: PRT
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Primer
158 <400> SEQUENCE: 10
159  Glu Leu Glu Val Leu Val Ser Thr Val
160   1               5
162 <210> SEQ ID NO: 11
163 <211> LENGTH: 507
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
167 <220> FEATURE:
168 <221> NAME/KEY: CDS
169 <222> LOCATION: (1)...(504)
170 <223> OTHER INFORMATION: 4
173 <400> SEQUENCE: 11
174  atg ttc tgg aag ctt tcc ctg tcc ttg ttc ctg gtg gcg gtg ctg gtg       48
175  Met Phe Trp Lys Leu Ser Leu Ser Leu Phe Leu Val Ala Val Leu Val
176   1               5                  10                  15
178  aag gtg gcg gaa gcc cgg aag aac cgg ccg gcg ggc gcc atc ccc tcg       96
179  Lys Val Ala Glu Ala Arg Lys Asn Arg Pro Ala Gly Ala Ile Pro Ser
180              20                  25                  30
182  cct tac aag gac ggc agc agc aac aac tcg gag aga tgg cag cac cag      144
183  Pro Tyr Lys Asp Gly Ser Ser Asn Asn Ser Glu Arg Trp Gln His Gln
184          35                  40                  45
186  atc aag gag gtg ctg gcc tcc agc cag gag gcc ctg gtg gtc acc gag      192
187  Ile Lys Glu Val Leu Ala Ser Ser Gln Glu Ala Leu Val Val Thr Glu
188      50                  55                  60
190  cgc aag tac ctc aag agt gac tgg tgc aag acg cag ccg ctg cgg cag      240
191  Arg Lys Tyr Leu Lys Ser Asp Trp Cys Lys Thr Gln Pro Leu Arg Gln
192   65                  70                  75                  80
194  acg gtg agc gag gag ggc tgc cgg agc cgc acc atc ctc aac cgc ttc      288
```

FYI: a primer is usually a nucleotide sequence.

see above

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```
195  Thr Val Ser Glu Glu Gly Cys Arg Ser Arg Thr Ile Leu Asn Arg Phe
196                  85                  90                  95
198  tgc tac ggc cag tgc aac tcc ttc tac atc ccg cgg cac gtg aag aag      336
199  Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro Arg His Val Lys Lys
200              100                 105                 110
202  gag gag gag tcc ttc cag tcc tgc gcc ttc tgc aag ccc cag cgc gtc      384
203  Glu Glu Glu Ser Phe Gln Ser Cys Ala Phe Cys Lys Pro Gln Arg Val
204          115                 120                 125
206  acc tcc gtc ctc gtg gag ctc gag tgc ccc ggc ctg gac cca ccc ttc      432
207  Thr Ser Val Leu Val Glu Leu Glu Cys Pro Gly Leu Asp Pro Pro Phe
208      130                 135                 140
210  cga ctc aag aaa atc cag aag gtg aag cag tgc cgg tgc atg tcc gtg      480
211  Arg Leu Lys Lys Ile Gln Lys Val Lys Gln Cys Arg Cys Met Ser Val
212  145                 150                 155                 160
214  aac ctg agc gac tcg gac aag cag tga                              507
215  Asn Leu Ser Asp Ser Asp Lys Gln
216                  165
218 <210> SEQ ID NO: 12
219 <211> LENGTH: 168
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapiens
223 <400> SEQUENCE: 12
224  Met Phe Trp Lys Leu Ser Leu Ser Leu Phe Leu Val Ala Val Leu Val
225   1               5                  10                  15
226  Lys Val Ala Glu Ala Arg Lys Asn Arg Pro Ala Gly Ala Ile Pro Ser
227              20                  25                  30
228  Pro Tyr Lys Asp Gly Ser Ser Asn Asn Ser Glu Arg Trp Gln His Gln
229          35                  40                  45
230  Ile Lys Glu Val Leu Ala Ser Ser Gln Glu Ala Leu Val Val Thr Glu
231      50                  55                  60
232  Arg Lys Tyr Leu Lys Ser Asp Trp Cys Lys Thr Gln Pro Leu Arg Gln
233  65                  70                  75                  80
234  Thr Val Ser Glu Glu Gly Cys Arg Ser Arg Thr Ile Leu Asn Arg Phe
235                  85                  90                  95
236  Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro Arg His Val Lys Lys
237              100                 105                 110
238  Glu Glu Glu Ser Phe Gln Ser Cys Ala Phe Cys Lys Pro Gln Arg Val
239          115                 120                 125
240  Thr Ser Val Leu Val Glu Leu Glu Cys Pro Gly Leu Asp Pro Pro Phe
241      130                 135                 140
242  Arg Leu Lys Lys Ile Gln Lys Val Lys Gln Cys Arg Cys Met Ser Val
243  145                 150                 155                 160
244  Asn Leu Ser Asp Ser Asp Lys Gln
245                  165
247 <210> SEQ ID NO: 13
248 <211> LENGTH: 48
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
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253 <223> OTHER INFORMATION: Primer
255 <400> SEQUENCE: 13
256 cagatagaat tcgccgccac catggtgtgg aagctttccc tgtccttg 48
258 <210> SEQ ID NO: 14
259 <211> LENGTH: 30
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Primer
266 <400> SEQUENCE: 14
267 cacgagaccg gtctgcttgt ccgagtcgct 30
269 <210> SEQ ID NO: 15
270 <211> LENGTH: 114
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Triple myc tag
277 <400> SEQUENCE: 15
278 gagcagaagc tgatatccga agaagacctc ggcggagagc agaagctcat aagtgaggaa 60
279 gacttgggcg gagagcagaa gcttatatcc gaagaagatc tcggaccgtg ataa 114
281 <210> SEQ ID NO: 16
282 <211> LENGTH: 52
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Primer
289 <400> SEQUENCE: 16
290 gagagacatg tctcggaaga accgtccggc tggcgccatc ccctcgcctt ac 52
292 <210> SEQ ID NO: 17
293 <211> LENGTH: 39
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Primer
300 <400> SEQUENCE: 17
301 gagagcggcc gctcattact gcttgtccga gtcgctcag 39
303 <210> SEQ ID NO: 18
304 <211> LENGTH: 9
305 <212> TYPE: PRT
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Mammalian
311 <400> SEQUENCE: 18
312 Arg Lys Tyr Leu Lys Ser Asp Trp Cys
313 1 5
315 <210> SEQ ID NO: 19
316 <211> LENGTH: 8
317 <212> TYPE: PRT
318 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/25/2003
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Input Set : **A:\REG660AZ.txt**
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 8,12,18
Seq#:2; N Pos. 6,9,12,21
Seq#:3; N Pos. 1,4,10,13,16
Seq#:4; N Pos. 1,7,10,19